Claims

1. An oligonucleotide selected from at least one of the DNA sequences designated SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, and/or SEQ ID NO: 6, or annealing equivalents thereof.

2. A oligonucleotide according to claim 1 which comprises a pair of PCR primers for identification of the genus *Cryptosporidium* to the genotypic and subgenotypic level, comprising at least 15 consecutive bases of the DNA sequence designated SEQ ID NO: 3 or an annealing equivalent thereof and a second primer comprising at least 15 consecutive bases of the DNA sequence designated SEQ ID NO: 4 or an annealing equivalent thereof, or at least 15 consecutive bases of the DNA sequence designated SEQ ID NO: 5 or an annealing equivalent thereof and a second primer comprising at least 15 consecutive bases of the DNA sequence designated SEQ ID NO: 6 or an annealing equivalent thereof.

3. An oligonucleotide according to claims 1 or 2 wherein said annealing equivalents comprise at least 15 nucleotides in length, and are adapted to anneal to a target sequence which is complementary to at least 15 consecutive bases of a primer selected from SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5 or SEQ ID NO: 6 at a temperature of 45 to 55°C in a buffer containing 1.5-7mM $MgCl_2$.

4. A method for the genotypic and subgenotypic identification of the genus *Cryptosporidium* in a sample, said method comprising the steps:

(a) providing a sample comprising genomic template DNA to be tested;

(b) providing a pair of PCR primers selected from the group consisting of:
primers comprising at least 15 consecutive bases of the DNA sequence designated SEQ ID NO: 3 or annealing equivalents thereof and SEQ ID NO: 4 or annealing equivalents thereof, or at least 15 consecutive bases of the DNA

sequence designated SEQ ID NO: 5 or annealing equivalents thereof and a second primer comprising at least 15 consecutive bases of the DNA sequence designated SEQ ID NO: 6 or an annealing equivalent thereof;

(c) amplifying by means of PCR a region of template DNA using said primer pair to produce one or more PCR products from the said sample, and thereafter analysing the PCR products so as to identify genotype and subgenotype *Cryptosporidium* in a sample.

5. A method according to claim 4 wherein said sample comprises a faecal sample.

6. A method according to claim 4 wherein genomic template DNA of one or more *Cryptosporidium* standards of known genotype, and optionally known subgenotype, are also provided and amplified, so as to provide a standard during identification of *Cryptosporidium* genotype and subgenotype.

7. A method according to claim 4 wherein PCR products are subject to electrophoretic separation

8. A method according to claim 1 wherein said electrophoretic separation comprises denaturing polyacrylamide gel electrophoresis (DGPE) or single-strand conformation polymorphism (SSCP) electrophoresis.